



## SEQUENCE LISTING

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 Mathur, Eric J.

<120> RECOMBINANT PHYTASES AND METHODS OF MAKING  
 AND USING THEM

<130> 09010-029011

<140> US 10/601,319

<141> 2003-06-20

<150> US 09/866,379

<151> 2001-05-24

<150> US 09/580,515

<151> 2000-05-25

<150> US 09/318,528

<151> 1999-05-25

<150> US 09/291,931

<151> 1999-04-13

<150> US 09/259,214

<151> 1999-03-01

<150> US 08/910,798

<151> 1997-08-13

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<212> DNA

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<220>

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<221> misc\_feature

<222> 216

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ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt				96
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	20	25	30	
gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg				144
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	35	40	45	
caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta				192
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val	50	55	60	
aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc				240
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	65	70	75	80
gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa				288
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys	85	90	95	
aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac				336
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	100	105	110	
gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct				384
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro	115	120	125	
gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat				432
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	130	135	140	
ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg				480
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala	145	150	155	160
aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac				528
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp	165	170	175	
ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt				576
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu	180	185	190	
aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa				624
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu	195	200	205	
agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc				672
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala	210	215	220	
gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg				720
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr	225	230	235	240

gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg	768
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp	
245 250 255	
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat	816
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His	
260 265 270	
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc	864
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser	
275 280 285	
cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat	912
Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His	
290 295 300	
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg	960
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu	
305 310 315 320	
ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg	1008
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu	
325 330 335	
gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt	1056
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
340 345 350	
ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag	1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
355 360 365	
tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat	1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
370 375 380	
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc	1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
385 390 395 400	
ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca	1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala	
405 410 415	
ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg	1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu	
420 425 430	
aga tct cat cac cat cac cat cac taa	1323
Arg Ser His His His His His His	
435 440	

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&lt;211&gt; 440

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 2

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			20					25					30		
Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr
		35					40					45			
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val
50						55					60				
Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu
65					70					75					80
Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys
			85						90					95	
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp
			100					105					110		
Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro
		115					120					125			
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp
130						135					140				
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala
145					150					155					160
Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp
			165						170					175	
Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu
		180						185					190		
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu
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Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala
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Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr
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		260					265						270		
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		275					280					285			
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Met	Ala	Ala	Leu	Thr	Pro	His
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Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu
305				310						315					320
Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu
			325						330					335	
Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly
		340					345						350		
Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln
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Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp
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Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr
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Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala
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Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu
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<221> misc\_feature  
<222> 403  
<223> n = A,T,C or G

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tgatgcggcg cattagcatc gcacagggca atcaataatg tcagatatga aaagcggaaa 180  
catatcgatg aaagcgatct taatcccatt tttatctctt ctgattccgt taaccccgca 240  
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tcatggtgtg cgtgctccaa ccaaggccac gcaactgatg caggatgtca ccccagacgc 360  
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aatggtcggt	cgccattcc	agtaattgac	gcatccgatac	g		1901

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&lt;211&gt; 1901

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 403

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 6

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ccacgaccgc	ggcatcactc	accgccagca	tcggcggcgt	atcgacaatc	accagatcgt	1860
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&lt;210&gt; 7

<211> 1901  
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 tgatgcggcg cattagcatc gcatcaggca atcaataatg tcagatatga aaagcggaaa 180  
 catatcg atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg 229  
           Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro  
           1                          5                          10  
  
 tta acc ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg 277  
 Leu Thr Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu  
   15                          20                          25                          30  
  
 gaa agt gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag 325  
 Glu Ser Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys  
                           35                          40                          45  
  
 gcc acg caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg 373  
 Ala Thr Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp  
                           50                          55                          60  
  
 ccg gta aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc 421  
 Pro Val Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala  
                           65                          70                          75  
  
 tat ctc gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg 469  
 Tyr Leu Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu  
                           80                          85                          90  
  
 gcg aaa aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat 517  
 Ala Lys Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp  
   95                          100                          105                          110  
  
 gtc gac gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg 565  
 Val Asp Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu  
                           115                          120                          125  
  
 gca cct gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt 613  
 Ala Pro Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser  
                           130                          135                          140  
  
 ccc gat ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat 661  
 Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp  
                           145                          150                          155  
  
 aac gcg aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att 709

Asn	Ala	Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	
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Ala	Asp	Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	
175					180				185					190		
gtg	ctt	aat	ttt	ccg	caa	tca	aac	ttg	tgc	ctt	aaa	cgt	gag	aaa	cag	805
Val	Leu	Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	
				195				200						205		
gac	gaa	agc	tgt	tca	tta	acg	cag	gca	tta	cca	tcg	gaa	ctc	aag	gtg	853
Asp	Glu	Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	
			210					215					220			
agc	gcc	gac	aat	gtc	tca	tta	acc	ggg	gcg	gta	agc	ctc	gca	tca	atg	901
Ser	Ala	Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	
		225					230					235				
ctg	acg	gag	ata	ttt	ctc	ctg	caa	caa	gca	cag	gga	atg	ccg	gag	ccg	949
Leu	Thr	Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	
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ggg	tgg	gga	agg	atc	acc	gat	tca	cac	cag	tgg	aac	acc	ttg	cta	agt	997
Gly	Trp	Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	
255					260				265					270		
ttg	cat	aac	gcg	caa	ttt	tat	ttg	cta	caa	cgc	acg	cca	gag	gtt	gcc	1045
Leu	His	Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	
				275					280					285		
cgc	agc	cgc	gcc	acc	ccg	tta	tta	gat	ttg	atc	aag	aca	gcg	ttg	acg	1093
Arg	Ser	Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Lys	Thr	Ala	Leu	Thr	
			290					295					300			
ccc	cat	cca	ccg	caa	aaa	cag	gcg	tat	ggg	gtg	aca	tta	ccc	act	tca	1141
Pro	His	Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	
		305					310					315				
gtg	ctg	ttt	atc	gcc	gga	cac	gat	act	aat	ctg	gca	aat	ctc	ggc	ggc	1189
Val	Leu	Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	
	320					325				330						
gca	ctg	gag	ctc	aac	tgg	acg	ctt	ccc	ggg	cag	ccg	gat	aac	acg	ccg	1237
Ala	Leu	Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	
335					340					345					350	
cca	ggg	ggg	gaa	ctg	gtg	ttt	gaa	cgc	tgg	cgt	cgg	cta	agc	gat	aac	1285
Pro	Gly	Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	
				355					360					365		
agc	cag	tgg	att	cag	gtt	tcg	ctg	gtc	ttc	cag	act	tta	cag	cag	atg	1333
Ser	Gln	Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	
			370					375					380			
cgt	gat	aaa	acg	ccg	ctg	tca	tta	aat	acg	ccg	ccc	gga	gag	gtg	aaa	1381
Arg	Asp	Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	



385	390	395	
ctg acc ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg			1429
Leu Thr Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser			
400	405	410	
ttg gca ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc			1477
Leu Ala Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys			
415	420	425	430
agt ttg taatgcataa aaaagagcat tcagttacct gaatgctctg aggctgatga			1533
Ser Leu			

caaacgaaga actgtctaata gcgtagaccg gaaaaggcgt tcacgccgca tccggccact	1593
ttcagttttc ctctttctcg gagtaactat aaccgtaata gttatagccg taactgtaag	1653
cggtgctggc gcgtttaatc acaccattga ggatagcgcc tttaatatattg acgcctgcct	1713
gttccagacg ctgcattgac aaactcacct ctttggcggg gttcaagcca aaacgcgcaa	1773
ccagcaggct ggtgccaaaca gaacgcccca cgaccgcggc atcactcacc gccagcatcg	1833
gcggcgatc gacaatcacc agatcgtaat ggtcgttcgc ccattccagt aattgacgca	1893
tccgatcg	1901

&lt;210&gt; 8

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 8

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr	
1 5 10 15	
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	
20 25 30	
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	
35 40 45	
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val	
50 55 60	
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
65 70 75 80	
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys	
85 90 95	
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
100 105 110	
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro	
115 120 125	
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	
130 135 140	
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala	
145 150 155 160	
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp	
165 170 175	
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu	
180 185 190	
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu	
195 200 205	
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala	
210 215 220	
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr	

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225          230          235          240
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
          245          250          255
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
          260          265          270
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
          275          280          285
Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His
          290          295          300
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
305          310          315          320
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
          325          330          335
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
          340          345          350
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
          355          360          365
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
          370          375          380
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
385          390          395          400
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
          405          410          415
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
          420          425          430

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&lt;210&gt; 9

&lt;211&gt; 1308

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; modified phytase enzyme

&lt;221&gt; CDS

&lt;222&gt; (1)...(1296)

&lt;400&gt; 9

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atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg tta acc      48
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
  1              5              10              15

ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt      96
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
          20              25              30

gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg      144
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
          35              40              45

caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta      192
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
          50              55              60

aaa ctg ggt gag ctg aca ccg cgc ggt ggt gag cta atc gcc tat ctc      240
Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
  65              70              75              80

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gga cat tac tgg cgt cag cgt ctg gta gcc gac gga ttg ctg cct aaa	288
Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys	
85 90 95	
tgt ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac	336
Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
100 105 110	
gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct	384
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro	
115 120 125	
gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat	432
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	
130 135 140	
ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg	480
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala	
145 150 155 160	
aac gtg act gac gcg atc ctc gag agg gca gga ggg tca att gct gac	528
Asn Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp	
165 170 175	
ttt acc ggg cat tat caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt	576
Phe Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu	
180 185 190	
aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa	624
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu	
195 200 205	
agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc	672
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala	
210 215 220	
gac tgt gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg	720
Asp Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr	
225 230 235 240	
gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg	768
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp	
245 250 255	
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat	816
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His	
260 265 270	
aac gcg caa ttt gat ttg cta caa cgc acg cca gag gtt gcc cgc agc	864
Asn Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser	
275 280 285	
cgc gcc acc ccg tta tta gat ttg atc aag aca gcg ttg acg ccc cat	912
Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His	
290 295 300	

cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gtg ctg 960  
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu  
 305 310 315 320

ttt atc gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg 1008  
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu  
 325 330 335

gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt 1056  
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly  
 340 345 350

ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag 1104  
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln  
 355 360 365

tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat 1152  
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp  
 370 375 380

aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc 1200  
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr  
 385 390 395 400

ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca 1248  
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala  
 405 410 415

ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg 1296  
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu  
 420 425 430

agatctcatc ta 1308

<210> 10

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> modified phytase enzyme

<400> 10

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr  
 1 5 10 15  
 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser  
 20 25 30  
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
 35 40 45  
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
 50 55 60  
 Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
 65 70 75 80  
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys  
 85 90 95  
 Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
 100 105 110

Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro
		115					120					125			
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp
	130					135					140				
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala
145					150					155					160
Asn	Val	Thr	Asp	Ala	Ile	Leu	Glu	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp
			165						170						175
Phe	Thr	Gly	His	Tyr	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu
		180						185					190		
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu
	195						200					205			
Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala
	210				215						220				
Asp	Cys	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr
225					230					235					240
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp
			245						250					255	
Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His
		260					265						270		
Asn	Ala	Gln	Phe	Asp	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser
	275						280					285			
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Lys	Thr	Ala	Leu	Thr	Pro	His
	290					295					300				
Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu
305					310					315					320
Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu
			325						330					335	
Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly
		340						345					350		
Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln
	355						360					365			
Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp
	370					375					380				
Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr
385					390					395					400
Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala
			405					410						415	
Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu
			420					425					430		